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August 10, 2004

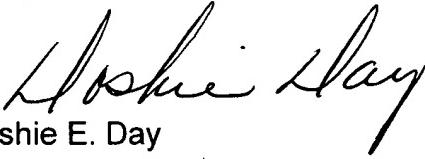
Linda S. Evans
Johnson & Johnson
One Johnson & Johnson Plaza
New Brunswick, NJ 08933-7003

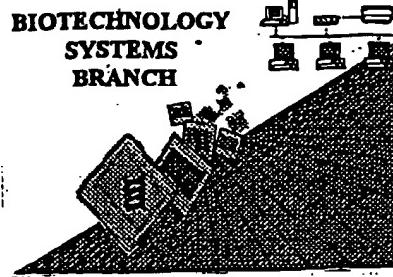
In re application of:
Darrow et al
No.: 10/015,989
Filed: December 10, 2001
For: Zymogen Activation System

In response to the petition received on February 26, 2004, to withdraw the holding of abandonment in the above application. A copy of the sequence list sent March 25, 2002, has not reached the application. Enclosed is a copy of the raw sequence listing error report.

Please submit these documents to complete the application.

Telephone inquiries concerning this matter may be directed to Doshie E. Day at (703) 308-3640.


Doshie E. Day
Program Management Assistant
Office Initial Patent Examination



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/015,989
Source: OIF
Date Processed by STIC: 1/3/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE: SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - cPAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

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Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/015,989</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII-text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <210>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <210>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n!	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,989

DATE: 01/03/2002
TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

7 <110> APPLICANT: DARROW, ANDREW
10 QI, JENSON
13 ANDRADE-GORDON, PATRICIA
19 <120> TITLE OF INVENTION: ZYMOGEN ACTIVATION SY
25 <130> FILE REFERENCE: ORT-1552
31 <140> CURRENT APPLICATION NUMBER: US/10/015,989
34 <141> CURRENT FILING DATE: 2001-12-10
40 <160> NUMBER OF SEQ ID NOS: 60
46 <170> SOFTWARE: PATENTIN VER. 2.0

see item 4 on
Error Summary
Sheet

Does Not Comply *ppr 1-12*
Corrected Diskette Needed

ERRORRED SEQUENCES

52 <210> SEQ ID NO: 1
55 <211> LENGTH: 361
58 <212> TYPE: DNA
61 <213> ORGANISM: ARTIFICIAL SEQUENCE
67 <220> FEATURE:
70 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
73 VECTORS.
79 <400> SEQUENCE: 1

E--> 82 gaattcacca ccatggacag caaagggtcg tcgcagaaat cccgcctgct 60 ← form
83 cctgctgctg 60

E--> 86 gtggtgtcaa atctactttt gtgccagggt gtggtctccg actacaagga 120 ← erra
87 cgacgacgac 120

E--> 90 gtggacgcgg ccgcgtttgc tgcccccttt gatgatgatg acaagatcgt
91 tgggggctat 180

E--> 94 gctctagata gcggccgcgtt cccttagtg agggtaatg ctgcagcag
95 acatgataag 240

E--> 98 atacattgt gagtttggac aaaccacaac tagaatgcag tgaaaaaaaat
99 gctttatttg 300

E--> 102 tgaatattgt gatgtatattg ctttatttg aaccattata agctgcaata
103 aacaagttga 360

106 c 361

112 <210> SEQ ID NO: 2
115 <211> LENGTH: 301
118 <212> TYPE: DNA
121 <213> ORGANISM: ARTIFICIAL SEQUENCE
127 <220> FEATURE:
130 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
133 VECTORS.
139 <400> SEQUENCE: 2

E--> 142 gaattcacca tgaatccact cctgatcctt acctttgtgg cggccgcgtct
143 tgctgcccc 60

E--> 146 ttgtatgatg atgacaagat cgtgggggc tattgtctag ataccctac
147 gatgtcccc 120

E--> 150 attacgccta gcggccgcgtt cccttagtg agggtaatg ctgcagcag

be in low
when sequence
60 ← form
120 ← erra
same for

FYI: Nucleotides must
be in lower-case letters
when Sequence Listing is
AL SEQUENCE: FUSION GENE in new
Sequence Rules
format

ccctgtc → 60 < format (see
caaggg → 120 < error item 1
gatcgt
gagcag
aaaaat
cgcaata

↓

error on Error Summary Sheet)

361

same format error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,989

DATE: 01/03/2002
TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

151 acatgataag 180
E--> 154 atacatttat gagttggac aaaccacaac tagaatgcag tgaaaaaaaaat
155 gctttatgg 240
E--> 158 taaaatgtt gatgttattt ctttatttgt aaccattata agctgcaata
159 aacaaggta 300
162 c
168 <210> SEQ ID NO: 3
171 <211> LENGTH: 484
174 <212> TYPE: DNA
177 <213> ORGANISM: ARTIFICIAL SEQUENCE
183 <220> FEATURE:
186 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
189 VECTORS.
195 <400> SEQUENCE: 3
E--> 198 gaattcacca ccatggacag caaaggatcg tcgcagaaat cccgcctgt
199 cctgctgtc 60
E--> 202 gtgggttcaa atctacttgc ttgtccagggt gtgggttccg actacaagg
203 cgacgacgac 120
E--> 206 gtggacgccc ccgcctttgc tggccctttt atcgaggggc gcattgtgga
207 gggctcgat 180
E--> 210 cttagatacc ctagatgtg cccgattacg ccgcatacata cccctacat
211 gtggccgatt 240
E--> 214 acggccctag ataccactac gatgtccccg attacgcgc tagataaccc
215 tacatgtgc 300
E--> 218 ccgattacgc ctagccggc cttcccttta gtgagggtta atgcttcgag
219 cagacatgt 360
E--> 222 aagatacatt gatgatgtt gacaaaccac aactagaatg cagtggaaaa
223 aatgctttat 420
E--> 226 ttgtgaaatt tgtatgtcta ttgttattt tgtaaccatt ataagctgca
227 ataaacaagt 480
230 tgac
236 <210> SEQ ID NO: 4
239 <211> LENGTH: 382
242 <212> TYPE: DNA
245 <213> ORGANISM: ARTIFICIAL SEQUENCE
251 <220> FEATURE:
254 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
257 VECTORS.
263 <400> SEQUENCE: 4
E--> 266 gaattcacca ccatggacag caaaggatcg tcgcagaaat cccgcctgt
267 cctgctgtc 60
E--> 270 gtgggttcaa atctacttgc ttgtccagggt gtgggttccg actacaagg
271 cgacgacgac 120
E--> 274 gtggacgccc ccgcctttgc tggccctttt gatgtatgt acaagatgt
275 tggggctac 180
E--> 278 aactgtctag acatcaccat caccatcaat agcgccgc tccctttatgt
279 gagggtaat 240
E--> 282 gttcgagca gacatgataa gatacattga tgagtttggaa caaaccacaa
283 cttagatgtc 300

-301 -

484

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,989

DATE: 01/03/2002
TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

E--> 286 tgaaaaaaaaa tgcttattt tgaaaatttg tgatgctatt gctttatttg
 287 taaccattat 360
 290 aagctgcaat aaacaagttg ac
 296 <210> SEQ ID NO: 5
 299 <211> LENGTH: 352
 302 <212> TYPE: DNA
 305 <213> ORGANISM: ARTIFICIAL SEQUENCE
 311 <220> FEATURE:
 314 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
 317 VECTORS.
 323 <400> SEQUENCE: 5

E--> 326 gaattcacca ccatggctt cctctggctc ctctcctgct gggccctct
 327 gggtaaccacc 60

E--> 330 ttccggctcg gggccccga ctacaaggac gacgacgacg cggccgcct
 331 tgctgcccc 120

E--> 334 ttgtatgatg atgacaagat cgttgggggc tatgctctag acatcaccat
 335 caccatcaact 180

E--> 338 agcggccgc tcccttagt gagggtaat gcttcgagca gacatgataa
 339 gatacatgta 240

E--> 342 tgagtggaa caaaccacaa ctagaatgca tgaaaaaaaaa tgctttattt
 343 tgaaaatttg 300

E--> 346 tgatgctatt gctttatttg taaccattat aagctgcaat aaacaagttg
 347 ac 352

353 <210> SEQ ID NO: 6
 356 <211> LENGTH: 385
 359 <212> TYPE: DNA
 362 <213> ORGANISM: ARTIFICIAL SEQUENCE
 368 <220> FEATURE:
 371 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
 374 VECTORS.
 380 <400> SEQUENCE: 6

E--> 383 gaattcacca ccatggctt cctctggctc ctctcctgct gggccctct
 384 gggtaaccacc 60

E--> 387 ttccggctcg gggccccga ctacaaggac gacgacgacg cggccgcct
 388 tgctgcccc 120

E--> 391 ttgtatgatg atgacaagat cgttgggggc tatgctctag ataccctac
 392 gatgtgcccc 180

E--> 395 attacggccgc tagacatcac catcaccatc actagggcc gcttccctt
 396 agtgagggtt 240

E--> 399 aatgtttcgaa gcagacatga taagatacat tgatgagttt ggacaaacca
 400 caactagaat 300

E--> 403 gcagtaaaaa aaatgtttt tttgtgaaat ttgtatgct attgctttat
 404 ttgttaaccat 360

407 tataagctgc aataaacaag ttgac

413 <210> SEQ ID NO: 7
 416 <211> LENGTH: 1169
 419 <212> TYPE: DNA
 422 <213> ORGANISM: ARTIFICIAL SEQUENCE
 428 <220> FEATURE:

382

385

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,989

DATE: 01/03/2002
TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

431 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
434 WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
440 <400> SEQUENCE: 7
E--> 443 gaattcaceca ccatggacag caaaggttcg tcgcagaaaat cccgcctgct
444 cctgctgctg 60
E--> 447 gtgggtgtcaa atctacttctt gtgccagggt gtggtctccg actacaagga
448 cgacgacgac 120
E--> 451 gtggacgccc cccgtcttgc tgcccccttt gatgatgatg acaagatcg
452 tgggggttat 180
E--> 455 gctctagagg cccgtcagtg gccctggcag gtcagcatca cctatgaagg
456 cgtccatgtg 240
E--> 459 tgtggtggtct ctctcggtc tgagcagtgg gtgctgtcag ctgctcactg
460 ctcccccagc 300
E--> 463 gagcaccaca aggaaggcta tgaggtcaag ctgggggccc accagctaga
464 ctcctactcc 360
E--> 467 gaggacgcca aggtcagcac cctgaaggac atcatcccc accccagcta
468 cctccaggag 420
E--> 471 ggctcccagg gcgcacattgc actcctccaa ctcagcagac ccatacacctt
472 ctccccgtac 480
E--> 475 atceggccca tctgcctccc tgcagccaaac gcctccttcc ccaacggcct
476 ccactgcact 540
E--> 479 gtaactggct ggggtcatgt ggccccctca gtgagcctcc tgacgcccac
480 gccactgcag 600
E--> 483 caactcgagg tgcctctgat cagtcgtgag acgtgttaact gcctgtacaa
484 catcgacgcc 660
E--> 487 aagectgagg agccgcacctt tgcaccaagag gacatgggtgt gtgctggcta
488 tgtggagggg 720
E--> 491 gcaaggacg cctgccaggg tgactctggg ggcccactct cctgcccgt
492 ggagggtctc 780
E--> 495 tggtaacctga cgggcattgt gagctggga gatgcctgtg gggcccgcaa
496 caggccttgt 840
E--> 499 gttacactc tggcctccag ctatgcctcc tggatccaaa gcaagggtgac
500 agaactccag 900
E--> 503 ctcgtgtgg tgccccaaac ccaggagtcc cagcccgaca gcaaccctcg
504 tggcagccac 960
E--> 507 ctggccttca gctctagaca tcaccatcac catcaactagc ggccgcttcc
508 ctttagttag 1020
E--> 511 gttaatgtc tgcagcagac atgataagat acattgtga gtttggacaa
512 accacaacta 1080
E--> 515 gaatgcagtg aaaaaaatgc ttatgttgaa aaatttgtga tgctattgt
516 ttatgttaa 1140
519 ccattataag ctgcataaaa caagttgac
525 <210> SEQ ID NO: 8
528 <211> LENGTH: 1142
531 <212> TYPE: DNA
534 <213> ORGANISM: ARTIFICIAL SEQUENCE
540 <220> FEATURE:
543 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
546 WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,989

DATE: 01/03/2002
TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

552 <400> SEQUENCE: 8
E--> 555 gaattcacca ccatgcttt cctctggctc ctctcctgtct gggccctcct
556 gggtaccacc 60
E--> 559 ttcggctgcg gggccccga ctacaaggac gacgacgacg cggccgcct
560 tgcgtcccc 120
E--> 563 ttgtatgtat atgacaagat cgttggggc tatgtcttag agggcggtca
564 gtggccctgg 180
E--> 567 caggtcagca tcacccatgaa aggcgtccat gtgtgtggtg gctcttcgt
568 gtcgtggcag 240
E--> 571 tgggtgtgt cagctgtca ctgttcccc agcgagcacc acaaggaagc
572 ctatgagggtc 300
E--> 575 aagctggggg cccaccagct agactcctac tccgaggacg ccaagggtcag
576 caccctgaag 360
E--> 579 gacatcatcc cccacccag ctacccctcag gagggctccc agggcgacat
580 tgcactctc 420
E--> 583 caactcagca gacccatcac cttctccgc tacatccggc ccatctgcct
584 ccctgcagcc 480
E--> 587 aacgccttcct tccccaacgg cctccactgc actgtcaactg gctggggtca
588 tgtggccccc 540
E--> 591 tcaagtggcc tcctgacgcc caagccactg cagcaactcg aggtgcctct
592 gatcagtcgt 600
E--> 595 gagacgtgtta actgcctgtt caacatcgac gccaaggctg aggagccgca
596 ctttgtccaa 660
E--> 599 gaggacatgg tgtgtgtgg ctatgtggag gggggcaagg acgcctgcca
600 gggtgactct 720
E--> 603 gggggcccac tctccctgcgg tgggggggt ctctgggtacc tgacgggcat
604 tgtgagtcgt 780
E--> 607 ggagatgcct gtggggcccg caacaggcct ggtgtgtaca ctctggcctc
608 cagctatgccc 840
E--> 611 tcttggatcc aaagcaaggt gacagaactc cagccctcggt tgggtggccca
612 aacccaggag 900
E--> 615 tcccagcccg acagcaacct ctgtggcagc cacctggcct tcagetctag
616 acatcaccat 960
E--> 619 caccatcaact agccggcgt tcccttttgt gagggtaat gcttcgagca
620 gacatgataa 1020
E--> 623 gatacattga tgagtttggaa caaaccacaa ctagaatgca gtaaaaaaaa
624 tgcattttttt 1080
E--> 627 gtgaaatttt tgatgttattt gctttatttg taaccattat aagctgcaat
628 aaacaagttt 1140
631 ac
637 <210> SEQ ID NO: 9
640 <211> LENGTH: 1049
643 <212> TYPE: DNA
646 <213> ORGANISM: ARTIFICIAL SEQUENCE
652 <220> FEATURE:
655 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
658 WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
664 <400> SEQUENCE: 9
E--> 667 gaattcacca ccatggacacg caaagggtcg tcgcagaaat cccgcctgtct

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,989

DATE: 01/03/2002
TIME: 15:41:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

668 cctgctgctg 60
E--> 671 gtgggtgtcaa atctactctt gtgccagggt gtgggtctccg actacaagga
672 cgacgacgac 120
E--> 675 gtggacgcgg ccgcctttgc tgcccccttt gatgatgatg acaagatcgt
676 tgggggtcac 180
E--> 679 aactgtctag aacccattc gcagccttgg cagggggcct tggccagg
680 ccagcaacta 240
E--> 683 ctctgtggcg gtgtccttgt aggtggcaac tgggtcctta cagctgccc
684 ctgtaaaaaaaa 300
E--> 687 ccgaaataca cagtacgcct gggagaccac agectacaga ataaagatgg
688 cccagagcaa 360
E--> 691 gaaatacctg tggttcagtc catcccacac ccctgctaca acagcagcga
692 tgtggaggac 420
E--> 695 cacaaccatg atctgatgct tcttcaactg cgtgaccagg catccctgg
696 gtccaaagtg 480
E--> 699 aagcccatca gcctggcaga tcattgcacc cagcctggcc agaagtgcac
700 cgtctcaggc 540
E--> 703 tggggactg tcaccagtcc ccgagagaat tttcctgaca ctctcaactg
704 tgcagaagta 600
E--> 707 aaaatcttc cccagaagaa gtgtgaggat gcttaccgg ggcagatcac
708 agatggcatg 660
E--> 711 gtctgtgcag gcagcagcaa aggggctgac acgtgccagg gcgattctgg
712 aggccccctg 720
E--> 715 gtgtgtgatg gtgcactcca gggcatcaca tcctgggct cagaccctg
716 tgggaggtcc 780
E--> 719 gacaaacctg gctctatac caacatctgc cgctacctgg actggatcaa
720 gaagatcata 840
E--> 723 ggcagcaagg gctctagaca tcaccatcac catcaactgc ggccgcttcc
724 cttagtgag 900
E--> 727 ggttaatgct tcgagcagac atgataagat acattgatga gtttggacaa
728 accacaacta 960
E--> 731 gaatgcagtg aaaaaaatgc tttatgttg aaatttgtga tgctattgct
732 ttatgttaa 1020
735 ccattataag ctgcaataaa caagttgac 1049
741 <210> SEQ ID NO: 10
744 <211> LENGTH: 1052
747 <212> TYPE: DNA
750 <213> ORGANISM: ARTIFICIAL SEQUENCE
756 <220> FEATURE:
759 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
762 WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
768 <400> SEQUENCE: 10
E--> 771 gaattcacca ccatggacag caaagggttcg tcgcagaaaat cccgcctgct
772 cctgctgctg 60
E--> 775 gtgggtgtcaa atctactctt gtgccagggt gtgggtctccg actacaagga
776 cgacgacgac 120
E--> 779 gtggacgcgg ccgcctttgc tgcccccttt gatgatgatg acaagatcgt
780 tgggggtcac 180
E--> 783 aactgtctag aaaagcactc ccagccctgg cagggcagccc tggccaggaa

RAW SEQUENCE LISTING
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Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

784 gacgcggcta 240
E--> 787 ctctgtgggg cgacgctcat cgccccaga tggctcctga cagcagccca
788 ctgcctcaag 300
E--> 791 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg
792 ctgtgagcag 360
E--> 795 acccggacag ccactgagtc cttcccccac cccggcttca acaacagcct
796 ccccaacaaa 420
E--> 799 gaccacccgca atgacatcat gctggtaag atggcatcgc cagtctccat
800 cacctggct 480
E--> 803 gtgcgacccc tcacctctc ctcacgctgt gtcactgctg gcaccagctg
804 cctcatttcc 540
E--> 807 ggctggggca gcacgtccag cccccagttt cgcctgcctc acaccttgcg
808 atgcgccaac 600
E--> 811 atcaccataa ttgagcacca gaagtgtgag aacgcctacc cccggcaacat
812 cacagacacc 660
E--> 815 atggtgtgtg ccagcgtgca ggaagggggc aaggactcct gccagggtga
816 ctccgggggc 720
E--> 819 cctctggctc gtaaccagtc tcttcaaggc attatctctt ggggccagga
820 tccgtgtgcg 780
E--> 823 atcaccggaa agcctgggtgt ctacacgaaa gtctgcaa atgtggactg
824 gatccaggag 840
E--> 827 acgatgaaga acaattctag acatcaccat caccatcaat agcggccgct
828 tcccttagt 900
E--> 831 gaggggtaat gcttcgagca gacatgataa gatacattga tgagtttgg
832 caaaccacaa 960
E--> 835 cttagaatgca gtgaaaaaaaa tgctttattt gtgaaatttg tgatgtatt
836 gctttatting 1020
839 taaccattat aagctgcaat aaacaagttt ac 1052
1067 <210> SEQ ID NO: 12
1070 <211> LENGTH: 319
1073 <212> TYPE: PRT
1076 <213> ORGANISM: ARTIFICIAL SEQUENCE
1082 <220> FEATURE:
1085 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE
1088 WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN
1094 <400> SEQUENCE: 12
1097 MET ALA PHE LEU TRP LEU LEU SER CYS TRP ALA LEU LEU GLY THR THR
1100 1 5 10 15 → Per Sequence
1106 PHE GLY CYS GLY VAL PRO ASP TYR LYS ASP ASP ASP ALA ALA ALA → Rules (1.822)
1109 20 25 30 → only the first
1115 LEU ALA ALA PRO PHE ASP ASP ASP LYS ILE VAL GLY GLY TYR ALA →
1118 35 40 45 →
1124 LEU GLU ALA GLY GLN TRP PRO TRP GLN VAL SER ILE THR TYR GLU GLY →
1127 50 55 60 →
1133 VAL HIS VAL CYS GLY GLY SER LEU VAL SER GLU GLN TRP VAL LEU SER →
1136 65 70 75 80 → letter of
1142 ALA ALA HIS CYS PHE PRO SER GLU HIS HIS LYS GLU ALA TYR GLU VAL → amino acid is
1145 85 90 95 → in upper-case.
1151 LYS LEU GLY ALA HIS GLN LEU ASP SER TYR SER GLU ASP ALA LYS VAL →
e.g. Met Ala

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Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

1154	100	105	110
1160	SER THR LEU LYS ASP ILE ILE PRO HIS PRO SER TYR LEU GLN GLU GLY		
1163	115	120	125
1169	SER GLN GLY ASP ILE ALA LEU LEU GLN LEU SER ARG PRO ILE THR PHE		
1172	130	135	140
1178	SER ARG TYR ILE ARG PRO ILE CYS LEU PRO ALA ALA ASN ALA SER PHE		
1181	145	150	155
1187	PRO ASN GLY LEU HIS CYS THR VAL THR GLY TRP GLY HIS VAL ALA PRO		
1190	165	170	175
1196	SER VAL SER LEU LEU THR PRO LYS PRO LEU GLN GLN LEU GLU VAL PRO		
1199	180	185	190
1205	LEU ILE SER ARG GLU THR CYS ASN CYS LEU TYR ASN ILE ASP ALA LYS		
1208	195	200	205
1214	PRO GLU GLU PRO HIS PHE VAL GLN GLU ASP MET VAL CYS ALA GLY TYR		
1217	210	215	220
1223	VAL GLU GLY GLY LYS ASP ALA CYS GLN GLY ASP SER GLY GLY PRO LEU		
1226	225	230	235
1232	SER CYS PRO VAL GLU GLY LEU TRP TYR LEU THR GLY ILE VAL SER TRP		
1235	245	250	255
1241	GLY ASP ALA CYS GLY ALA ARG ASN ARG PRO GLY VAL TYR THR LEU		more up
E-->	1242 ALA		
E-->	1245 260	265	270
	SER SER TYR ALA SER TRP ILE GLN SER LYS VAL THR GLU LEU GLN PRO		
E-->	1254 275	280	285
	ARG VAL VAL PRO GLN THR GLN GLU SER GLN PRO ASP SER ASN LEU CYS		
E-->	1263 290	295	300
	GLY SER HIS LEU ALA PHE SER SER ARG HIS HIS HIS HIS HIS HIS		
E-->	1272 305	310	315
	2409 <210> SEQ ID NO: 35		
	2412 <211> LENGTH: 55		
	2415 <212> TYPE: DNA		
	2418 <213> ORGANISM: ARTIFICIAL SEQUENCE		
	2424 <220> FEATURE:		
	2427 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:		
	2430 OLIGONUCLEOTIDE		
	2436 <400> SEQUENCE: 35		
E-->	2439 aattcacaccatgggttccctctggctccatctgtggcgtggcgatggcccttcgtg		more up - see item 1 on Env summary sheet
	2440 ggtac 55		
	2446 <210> SEQ ID NO: 36		
	2449 <211> LENGTH: 47		
	2452 <212> TYPE: DNA		
	2455 <213> ORGANISM: ARTIFICIAL SEQUENCE		
	2461 <220> FEATURE:		
	2464 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:		
	2467 OLIGONUCLEOTIDE		
	2473 <400> SEQUENCE: 36		
E-->	2476 ccaggaggc ccagcaggag aggagccaga ggaaagccat ggtggtg		same env
	2477 47		
	2483 <210> SEQ ID NO: 37		

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Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

2486 <211> LENGTH: 45
2489 <212> TYPE: DNA
2492 <213> ORGANISM: ARTIFICIAL SEQUENCE
2498 <220> FEATURE:
2501 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2504 OLIGONUCLEOTIDE
2510 <400> SEQUENCE: 37
E--> 2513 caccttcggc tgcggggtcc ccgactacaa ggacgacgac gacgc *same*
2514 45
2520 <210> SEQ ID NO: 38
2523 <211> LENGTH: 53
2526 <212> TYPE: DNA
2529 <213> ORGANISM: ARTIFICIAL SEQUENCE
2535 <220> FEATURE:
2538 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2541 OLIGONUCLEOTIDE
2547 <400> SEQUENCE: 38
E--> 2550 ggccgcgtcg tcgtcgctt tgtagtcggg gaccccgca gccaagggtgg *same*
2551 tac 53
2629 <210> SEQ ID NO: 41
2632 <211> LENGTH: 55
2635 <212> TYPE: DNA
2638 <213> ORGANISM: ARTIFICIAL SEQUENCE
2644 <220> FEATURE:
2647 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2650 OLIGONUCLEOTIDE
2656 <400> SEQUENCE: 41
E--> 2659 ggccgcgtttt gctgccccct ttgatgatga tgacaagatc gttgggggtt *same*
2660 atgct 55
2666 <210> SEQ ID NO: 42
2669 <211> LENGTH: 55
2672 <212> TYPE: DNA
2675 <213> ORGANISM: ARTIFICIAL SEQUENCE
2681 <220> FEATURE:
2684 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2687 OLIGONUCLEOTIDE
2693 <400> SEQUENCE: 42
E--> 2696 ctagagcata gcccccaacg atcttgcat catcataaaa gggggcagca *same*
2697 agagc 55
2703 <210> SEQ ID NO: 43
2706 <211> LENGTH: 55
2709 <212> TYPE: DNA
2712 <213> ORGANISM: ARTIFICIAL SEQUENCE
2718 <220> FEATURE:
2721 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2724 OLIGONUCLEOTIDE
2730 <400> SEQUENCE: 43
E--> 2733 ggccgcgtttt gctgccccct ttgatgatga tgacaagatc gttgggggtt *same*
2734 attgt 55

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Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

2740 <210> SEQ ID NO: 44
2743 <211> LENGTH: 55
2746 <212> TYPE: DNA
2749 <213> ORGANISM: ARTIFICIAL SEQUENCE
2755 <220> FEATURE:
2758 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2761 OLIGONUCLEOTIDE
2767 <400> SEQUENCE: 44
E--> 2770 ctagacaata gcccccaacg atcttgtcat catcatcaa gggggcagca *same*
2771 agagc 55
2777 <210> SEQ ID NO: 45
2780 <211> LENGTH: 52
2783 <212> TYPE: DNA
2786 <213> ORGANISM: ARTIFICIAL SEQUENCE
2792 <220> FEATURE:
2795 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2798 OLIGONUCLEOTIDE
2804 <400> SEQUENCE: 45
E--> 2807 ggccgcctt gctgcccctt ttatcgaggg gcgcatttg gagggctcgg *same*
2808 at 52
2814 <210> SEQ ID NO: 46
2817 <211> LENGTH: 52
2820 <212> TYPE: DNA
2823 <213> ORGANISM: ARTIFICIAL SEQUENCE
2829 <220> FEATURE:
2832 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:
2835 OLIGONUCLEOTIDE
2841 <400> SEQUENCE: 46
E--> 2844 cttagatccga gccctccaca atgcgcctt cgataaaggg ggcagcaaga *same*
2845 gc 52
3280 <210> SEQ ID NO: 54
3283 <211> LENGTH: 284
3286 <212> TYPE: PRT
3289 <213> ORGANISM: ARTIFICIAL SEQUENCE
3295 <220> FEATURE:
3298 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: HUMAN MH2
3301 PROTEASE IN PFEK ZYMOGEN VECTOR
3307 <400> SEQUENCE: 54
3310 MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU
3313 1 5 10 15
3319 VAL VAL SER ASN LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS
3322 20 25 30
3328 ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP
3331 35 40 45
3337 ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU PRO HIS SER GLN
3340 50 55 60
3346 PRO TRP GLN ALA ALA LEU VAL MET GLU ASN GLU LEU PHE CYS SER GLY
3349 65 70 75 80
3355 VAL LEU VAL HIS PRO GLN TRP VAL LEU SER ALA ALA HIS CYS PHE GLN

*please
edit
anso and
letters*

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Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

3358	85	90	95
3364	ASN SER TYR THR ILE GLY LEU GLY LEU HIS SER LEU GLU ALA ASP GLN		
3367	100	105	110
3373	GLU PRO GLY SER GLN MET VAL GLU ALA SER LEU SER VAL ARG HIS PRO		
3376	115	120	125
3382	GLU TYR ASN ARG PRO LEU LEU ALA ASN ASP LEU MET LEU ILE LYS LEU		
3385	130	135	140
3391	ASP GLU SER VAL SER GLU SER ASP THR ILE ARG SER ILE SER ILE ALA		
3394	145	150	155
3400	SER GLN CYS PRO THR ALA GLY ASN SER CYS LEU VAL SER GLY TRP GLY		
3403	165	170	175
3409	LEU LEU ALA ASN GLY ARG MET PRO THR VAL LEU GLN CYS VAL ASN		
E--> 3410	VAL		
E--> 3413	180	185	190
3419	SER VAL VAL SER GLU GLU VAL CYS SER LYS LEU TYR ASP PRO LEU TYR		
E--> 3422	195	200	205
3428	HIS PRO SER MET PHE CYS ALA GLY GLY HIS ASP GLN LYS ASP SER		
E--> 3431	210	215	220
3437	CYS ASN GLY ASP SER GLY GLY PRO LEU ILE CYS ASN GLY TYR LEU GLN		
E--> 3440	225	230	235
3446	GLY LEU VAL SER PHE GLY LYS ALA PRO CYS GLY GLN VAL GLY VAL PRO		
E--> 3449	245	250	255
3455	GLY VAL TYR THR ASN LEU CYS LYS PHE THR GLU TRP ILE GLU LYS THR		
E--> 3458	260	265	270
3464	VAL GLN ALA SER SER ARG HIS HIS HIS HIS HIS HIS		
E--> 3467	275	280	

3608 <210> SEQ ID NO: 59
 3611 <211> LENGTH: 1103
 3614 <212> TYPE: DNA
 3617 <213> ORGANISM: ARTIFICIAL SEQUENCE
 3623 <220> FEATURE:
 3626 <223> OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: NUCLEIC ACID
 3629 SEQUENCE OF HUMAN PROTEASE F IN CFEK2 ZYMOGEN
 3632 VECTOR
 3638 <400> SEQUENCE: 59

E--> 3641	gaattcacca	ccatggctt	cctctggctc	ctcttcgtct	ggccctct
3642	gggttaccacc	60			
E--> 3645	ttcggctcg	gggtccccga	ctacaaggac	gacgacgacg	cgccgcgtct
3646	tgctgcccc	120			
E--> 3649	tttgatgatg	atgacaagat	cgttggggc	tatgtcttag	aactcggcg
3650	ttggccgtgg	180			
E--> 3653	caggggagcc	tgcgcctgtg	ggattccac	gtatgcggag	tgagcctgct
3654	cagccacccg	240			
E--> 3657	ttggcactca	cggccgcga	ctgcttgaa	acctatagtg	accttagtga
3658	tccctccggg	300			
E--> 3661	tggatggccc	agtttgccca	gctgacttcc	atgccatct	tctggagcct
3662	gcaggcctac	360			
E--> 3665	tacaaccgtt	acttcgtatc	aatatctat	ctgagccctc	gctacacctgg
3666	gaattcaccc	420			

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E--> 3669 tatgacattt ccttggtaaa gctgtctgca cctgtcaccc acactaaaca
3670 catccagccc 480
E--> 3673 atctgtctcc aggcctccac attttagttt gagaaccgga cagactgctg
3674 ggtgactggc 540.
E--> 3677 tgggggtaca tcaaagagga tgaggcactg ccatactcccc acaccctcca
3678 ggaagttcag 600.
E--> 3681 gtcgccatca taaaacaactc tatgtgcaac caccctttcc tcaagtacag
3682 ttcccgcaag 660
E--> 3685 gacatctttg gagacatggt ttgtgctggc aatgcccag gcgggaagga
3686 tgcctgtttc 720
E--> 3689 ggtgactcag gtggaccctt ggcctgttaac aagaatggac tgtggtatca
3690 gattggatgc 780
E--> 3693 gtgagctggg gagtggttgc tggtcggccc aatcgccccg gtgtctacac
3694 caatatcagc 840
E--> 3697 caccactttt agtggatcca gaagctgatg gcccagatgt gcatgtccca
3698 gcccagacccc 900
E--> 3701 tcctggtcta gacatcacca tcaccatcac tagcggccgc ttccctttag
3702 tgagggttaa 960
E--> 3705 tgcttcgagc agacatgata agatacattt atgagtttgg acaaaccaca
3706 actagaatgc 1020
E--> 3709 agtggaaaaaa atgctttattt tgtgaaattt gtgatgtat tgccttattt
3710 gtaaccatttta 1080
3713 taagctgcaa taaacaagtt gac

1103

*same
error*

→ Follow the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

L:31 M:270 C: Current Application Number differs, Replaced Application Number
L:34 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
L:82 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
M:254 Repeated in SeqNo=1
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:2
M:112 Repeated in SeqNo=2
M:254 Repeated in SeqNo=2
L:198 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:3
M:112 Repeated in SeqNo=3
M:254 Repeated in SeqNo=3
L:266 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:4
M:112 Repeated in SeqNo=4
M:254 Repeated in SeqNo=4
L:326 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:5
M:112 Repeated in SeqNo=5
M:254 Repeated in SeqNo=5
L:383 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:6
M:112 Repeated in SeqNo=6
M:254 Repeated in SeqNo=6
L:443 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:7
M:112 Repeated in SeqNo=7
M:254 Repeated in SeqNo=7
L:555 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:8
M:112 Repeated in SeqNo=8
M:254 Repeated in SeqNo=8
L:667 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:9
M:112 Repeated in SeqNo=9
M:254 Repeated in SeqNo=9
L:771 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:10
M:112 Repeated in SeqNo=10
M:254 Repeated in SeqNo=10
L:1242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:1719 M:112 C: (48) String data converted to lower case,
L:1755 M:112 C: (48) String data converted to lower case,
L:1791 M:112 C: (48) String data converted to lower case,
L:1827 M:112 C: (48) String data converted to lower case,
L:1863 M:112 C: (48) String data converted to lower case,
L:1899 M:112 C: (48) String data converted to lower case,
L:1935 M:112 C: (48) String data converted to lower case,
L:1971 M:112 C: (48) String data converted to lower case,
L:2007 M:112 C: (48) String data converted to lower case,
L:2043 M:112 C: (48) String data converted to lower case,
L:2079 M:112 C: (48) String data converted to lower case,
L:2115 M:112 C: (48) String data converted to lower case,
L:2151 M:112 C: (48) String data converted to lower case,

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Input Set : A:\ES.txt
Output Set: N:\CRF3\01032002\J015989.raw

L:2187 M:112 C: (48) String data converted to lower case,
L:2223 M:112 C: (48) String data converted to lower case,
L:2259 M:112 C: (48) String data converted to lower case,
L:2295 M:112 C: (48) String data converted to lower case,
L:2331 M:112 C: (48) String data converted to lower case,
L:2367 M:112 C: (48) String data converted to lower case,
L:2403 M:112 C: (48) String data converted to lower case,
L:2439 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:35
M:112 Repeated in SeqNo=35
L:2476 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:36
M:112 Repeated in SeqNo=36
L:2513 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:37
M:112 Repeated in SeqNo=37
L:2550 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:38
M:112 Repeated in SeqNo=38
L:2587 M:112 C: (48) String data converted to lower case,
L:2623 M:112 C: (48) String data converted to lower case,
L:2659 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:41
M:112 Repeated in SeqNo=41
L:2696 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:42
M:112 Repeated in SeqNo=42
L:2733 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:43
M:112 Repeated in SeqNo=43
L:2770 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:44
M:112 Repeated in SeqNo=44
L:2807 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:45
M:112 Repeated in SeqNo=45
L:2844 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:46
M:112 Repeated in SeqNo=46
L:2881 M:112 C: (48) String data converted to lower case,
L:2917 M:112 C: (48) String data converted to lower case,
L:2953 M:112 C: (48) String data converted to lower case,
L:2989 M:112 C: (48) String data converted to lower case,
L:3025 M:112 C: (48) String data converted to lower case,
L:3061 M:112 C: (48) String data converted to lower case,
L:3410 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54
M:332 Repeated in SeqNo=54
L:3503 M:112 C: (48) String data converted to lower case,
L:3641 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:59
M:254 Repeated in SeqNo=59
L:3752 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:60
M:254 Repeated in SeqNo=60

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